WHAT IS CLAIMED IS:

1. A composition comprising the *E. coli* MurG protein in crystalline form.

2. A composition comprising a MurG protein in crystalline form.

3. A three dimensional structure of the crystalline form of an *E. coli* MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 1.

4. A three dimensional structure of the crystalline form of a MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 1.

5. A three dimensional structure of the α-carbon backbone of the crystalline form of an *E. coli* MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 2.

6. A three dimensional structure of the α-carbon backbone and conserved amino acid residues of an *E .coli* MurG protein, wherein the three dimensional structure substantially conforms to the atomic coordinates represented in Table 3.

7. A three dimensional structure of a donor nucleotide binding site of a MurG protein wherein the three dimensional structure structure of the donor nucleotide binding site substantially conforms to the atomic coordinates in Table 4.

8. The three dimensional structure of claim 7, wherein the donor nucleotide is UDP-GlcNAc.

9. A three dimensional structure of an acceptor binding site of a MurG protein substantially conforming to the atomic coordinates in Table 5.

10. A three dimensional structure of a membrane association site of a MurG protein substantially conforming to the atomic coordinates in Table 6.

11. A three-dimensional computer image of the three-dimensional structure of a MurG protein.

12. The image of claim 11, wherein the structure substantially conforms with the three-dimensional coordinates listed in Table 1.

13. The image of claim 11, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 1 are analyzed on a computer using a graphical display software

program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

14. The image of claim 11, wherein the three-dimensional computer image is represented by a two dimensional image selected from the group consisting of Fig. 2a, 3a, or 4c.

15. The image of claim 11, wherein the three-dimensional computer image is used to design a compound.

16. A three dimensional computer image of the three dimensional structure of the α-carbon backbone of a MurG protein.

17. The image of claim 16, wherein the structure substantially conforms with the three-dimensional coordinates listed in Table 2.

18. The image of claim 16, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 2 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

19. The image of claim 16, wherein the three-dimensional computer image is used to design a compound.

20. A three dimensional image of the three dimensional image of an α-carbon backbone and conserved amino acid residues of a MurG protein.

21. The image of claim 20, wherein the structure substantially conforms with the three-dimensional coordinates in Table 3.

22. The image of claim 21, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 3 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

23. The image of claim 21, wherein the three-dimensional computer image is used to design a compound.

24. A three-dimensional computer image of the three-dimensional structure of a donor nucleotide binding site of a MurG protein.

25. The image of claim 24, wherein the structure substantially conforms with the three-dimensional coordinates in Table 4.

26. The image of claim 24, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 4 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

27. The image of claim 24, wherein the three-dimensional computer image is represented by a two dimensional image selected from the group consisting of Fig. 3c, 4a or 4b.

28. The image of claim 24, wherein the three-dimensional computer image is used to design a compound.

29. A three-dimensional computer image of the three-dimensional structure of an acceptor binding site of a MurG protein.

30. The image of claim 29, wherein the structure substantially conforms with the three-dimensional coordinates Table 5.

31. The image of claim 29, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 5 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

32. The image of claim 29, wherein the three-dimensional computer image is represented by the two dimensional image of Fig. 4a.

33. The image of claim 29, wherein the three-dimensional computer image is used to design a compound.

34. A three-dimensional computer image of the three-dimensional structure of a membrane association site of a MurG protein.

35. The image of claim 34, wherein the structure substantially conforms with the three-dimensional coordinates Table 6.

36. The image of claim 34, wherein the computer image is that is generated when a set of three-dimensional coordinates comprising the three-dimensional coordinates represented in Table 6 are analyzed on a computer using a graphical display software

program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

37. The image of claim 34, wherein the three-dimensional computer image is represented by the two dimensional image of Fig. 4a.

38. The image of claim 34, wherein the three-dimensional computer image is used to design a compound.

39. A computer readable medium encoded with a set of three-dimensional coordinates of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 1, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

40. A computer readable medium encoded with a set of three-dimensional coordinates of an α-carbon backbone of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 2, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

41. A computer readable medium encoded with a set of three-dimensional coordinates of an α-carbon backbone and conserved amino acid residues of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 3, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

42. A computer readable medium encoded with a set of three-dimensional coordinates of a donor nucleotide binding site of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 4, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

43. A computer readable medium encoded with a set of three-dimensional coordinates of an acceptor binding site of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 5, wherein using

a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

44. A computer readable medium encoded with a set of three-dimensional coordinates of a membrane association site of a MurG protein having a three-dimensional structure that substantially conforms to the atomic coordinates of Table 5, wherein using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing said electronic file as a three dimensional image.

45. A method for identifying a potential inhibitor of a UDP-glycosyltransferase enzyme, the method comprising the steps of:

a. using a three-dimensional structure of UDP-glycosyltransferase enzyme as defined by atomic coordinates of UDP-glycosyltransferase enzyme according to FIG. 5;

b. employing said three-dimensional structure to design or select said potential inhibitor;

c. synthesizing said potential inhibitor; and

d. contacting said potential inhibitor with said UDP-glycosyltransferase enzyme in the presence of a substrate to test the ability of said potential inhibitor to inhibit said UDP-glycosyltransferase enzyme.

46. The method according to claim 45, wherein said potential inhibitor is selected from a database.

47. The method according to claim 45, wherein said potential inhibitor is designed de novo.

48. The method according to claim 45, wherein said potential inhibitor is designed from a known inhibitor.

49. The method according to claim 45, wherein said step of employing said three-dimensional structure to design or select said potential inhibitor comprises the steps of:

a. identifying chemical entities or fragments capable of associating with UDP-glycosyltransferase enzyme; and

b. assembling the identified chemical entities or fragments into a single molecule to provide the structure of said potential inhibitor.

50. The method according to claim 45, wherein the potential inhibitor is a competitive inhibitor of mutant UDP-glycosyltransferase enzyme.

51. The method according to claim 45, wherein said potential inhibitor is a non-competitive or uncompetitive inhibitor of mutant UDP-glycosyltransferase enzyme.

52. A model of a UDP-glycosyltransferase, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 1.

53. The model of claim 52, wherein the structure substantially conforms to the atomic coordinates and B-values represented by Table 1.

54. The model of claim 52, wherein the structure is monomeric.

55. The model of claim 52, wherein at least about 50% of the structure has an average root-mean-square deviation (RMDS) of less than about 2.5 Å for backbone atoms in secondary structure elements in each domain of the structure.

56. The model of claim 52, wherein the MurG protein comprises an amino acid sequence that is at least about 25% identical to the amino acid sequence of the *E. coli* MurG protein.

57. The model of claim 52, wherein the MurG protein comprises an amino acid sequence that is at least about 40% identical to the amino acid sequence of the *E. coli* MurG protein.

58. The model of claim 52, wherein the MurG protein comprises an amino acid sequence that is at least about 60% identical to the amino acid sequence of the *E. coli* MurG protein.

59. The model of claim 52, wherein the MurG protein comprises an amino acid sequence selected from the group consisting of the amino acid sequence of a MurG protein from *Escherichia coli, Bacillus subtilis, Aquefex aeolicus, Borrelia burgdorferi, Chlamydia pneumoniae, Chlamydia trachomatis, Enterococcus faecais, Enterococcus hirae, Haemophilus influenzae, Helicobacter pylori J99, Helicobacter pylori, Mycobacterium tuberculosis, Porphyromonas gingivalis, Rickettsia prowazekii,Streptomyces coelicolor, Streptomyces collinus, Streptococcus pneumoniae, Synechocystis* sp. (strain PCC6803), *Thermotoga maritime,* and *Treponema pallidum*, a mutant of any of the amino acid sequences, and a variants of any of the amino acid sequences.

60. The model of claim 52, wherein the MurG protein comprises an amino acid sequence selected from the group consisting of the amino acid sequences of MurG proteins as deposited in the NCBI database and identified with Accession Nos. CAB51993, A71316, E70579, C71699, F70195, A43727, JC1275, BVECMG, CEECAM, O83535, Q9ZK59, CAB85280, AAF39020, BAA18775, AAD26629, CAB73295, P37585, Q9ZHA9, Q9ZHDC0, Q9ZBA5, Q9X4H4, Q9WY74, P74657, O06224, Q9Z702, O84766, O69552, )67238, O51708, O25770, O07670, O07109, P45065, CAB66324, AAC68356, AAF06830, P18579, P17443, P17952, P16457, P07862, AAE23178, AAD53936, CAA18668, CAA38869, CAA38868, CAA38867, CAA38866, AAD08196, BAA01453, BAA01455, BAA01454, AAD19042, CAA45558, CAA74235, AAD10537, AAD06652, AAC95450, CAA14869, AAC73201, AAC65509, AAC67113, AAC45636, CAB08640, AAC22793, AAC07193, BAA24357, CAB13395, BAA01355, AAB35538, 1904153C, 1808265B, 1808265A, CAA36866, CAA36869, CAA36868, CAA36867, CAA36776, and AAA99436.

61. The model of claim 52, wherein the MurG protein comprises an amino acid sequence obtained from an organism selected from the group consisting of bacteria, small pathogenic organisms, cyano bacteria, higher-order bacteria, spirochetes and thermal stable bacteria.

62. The model of claim 52, wherein the MurG protein comprises an amino acid sequence obtained from an organism selected from the group consisting of *Escherichia coli, Bacillus subtilis, Aquefex aeolicus, Borrelia burgdorferi, Chlamydia pneumoniae, Chlamydia trachomatis, Enterococcus faecais, Enterococcus hirae, Haemophilus influenzae, Helicobacter pylori J99, Helicobacter pylori, Mycobacterium tuberculosis, Porphyromonas gingivalis, Rickettsia prowazekii,Streptomyces coelicolor, Streptomyces collinus, Streptococcus pneumoniae, Synechocystis* sp. (strain PCC6803), *Thermotoga maritime,* and *Treponema pallidum.*

63. The model of claim 52, wherein the MurG protein is a structural homologue of the *E. coli* MurG protein.

64. The model of claim 52, wherein the structure comprises an n-terminal and C-terminal domain connected by a covalent peptide linker, and wherein each domain has an alpha/beta fold.

65. The model of claim 52, wherein the RMSD is less than 2.5 Å over at least 80 aligned C-alpha atoms in each domain.

66. The model of claim 52, wherein the N-terminal domain comprises two glycine rich loops.

67. The model of claim 66, wherein the amino acid sequence of the two glycine rich loops comprises GGTGGH and G-GGYVSG.

68. The model of claim 52, wherein the C-terminal domain comprises one glycine rich loop.

69. The model of claim 68, wherein the glycine rich loop comprises the amino acid sequence GGSQGAR or GGS-GAR.

70. The model of claim 52, wherein the atomic coordinates are generated by the method comprising the steps of:

(a) providing a MurG protein in crystalline form;

(b) generating an electron-density map of the crystalline MurG protein; and

(c) analyzing the electron-density map to produce the atomic coordinates.

71. The model of claim 70, wherein the crystalline MurG protein is produced by a method comprising the steps of:

(a) combining MurG protein with UDP-GlcNAc ,and

(b) inducing crystal formation to produce said crystalline MurG protein.

72. The model of claim 70, wherein the crystalline MurG protein is produced by the hanging drop method in which MurG in buffer is at a concentration of at least 5 ug/ml and is combined with a reservoir solution and crystallizes.

73. The model of claim 72, wherein the buffer has a pH range from about 6.5 to about 9.0, and a buffer concentration range from about 10 mM to about 200 mM.

74. The model of 73, wherein the buffer is a Tris or a Hepes buffer, having a pH from about 7.0 to about 8.5.

75. The model of 74, wherein the buffer has a pH of about 7.9.

76. The model of claim 73, wherein the buffer further comprises at least one salt, chelating agent, or reducing agent.

77. The model of claim 72, wherein the reservoir solution has a pH range from about 5.0 to about 9.0 and the buffer concentration ranges from about 10 mM to about 1M.

78. The model of claim 77, wherein the reservoir solution further comprises at least one suitable precipitant, a detergent, and a reducing agent.

79. The model of claim 78, wherein the reservoir solution comprises a NaMES or sodium citrate buffer having a pH from about 6.0 to about 7.0.

80. The model of claim 79, wherein the buffer has a pH of about 6.5.

81. The model of claim 78, wherein the precipitant is selected from the group consisting of ammonium sulfate and sodium potassium tartrate.

82. The model of 78, wherein the detergent is TritonX-100.

83. The model of 78, wherein the reducing agent is DTT, DTE or beta-mercaptoethanol.

84. The model of claim 71, wherein the MurG protein and the UDP-GlcNAc are in a 1:3 molar ratio.

85. The model of claim 71, wherein the buffer comprises 0.1 M NaMES, pH6.5, 0.9M $(NH_4)_2SO_4$, 0.4% TRITON X-100®, and 10 mM dithiothreitol (DTT).

86. The model of claim 71, wherein the step of generating an electron-density map comprises analyzing the crystalline MurG protein by X-ray diffraction.

87. The model of claim 70, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.

88. A model of a donor nucleotide binding site of a UDP-glycosyltransferase (MurG) protein, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 4.

89. The model of claim 88, wherein the donor nucleotide binding site is located within the MurG C-terminal domain.

90. The model of claim 88, wherein the structure substantially conforms to the atomic coordinates and B-values of Table 4.

91. The model of claim 88, wherein at least about 50% of the structure has an average root-mean-square (RMSD) of less than about 2.5Å for the conserved amino acid residues for the donor nucleotide binding site of the E. coli MurG.

92. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 70% identical to the conserved amino acid residues of the donor nucleotide binding site of E. coli MurG.

93. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 80% identical to the conserved amino acid residues of the donor nucleotide binding site of the E. coli MurG.

94. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 90% identical to the conserved amino acid residues of the donor nucleotide binding site of the E. coli MurG.

95. The model of claim 88, wherein the donor nucleotide binding site comprises an amino acid sequence that is at least about 95% identical to the conserved amino acid residues of the donor nucleotide binding site of the E. coli MurG.

96. The model of claim 88, wherein the atomic coordinates are generated by a method comprising the steps of:

a) providing a Murg protein in a crystalline form:

b) generating an electron-density map of said crystalline MurG protein; and

c) analyzing the electron-density map to produce the atomic coordinates.

97. The model of claim 88, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.

98. A model of an acceptor binding site of a UDP-glycosyltransferase (MurG) protein, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 5 .

99. The model of claim 98, wherein the structure substantially conforms to the atomic coordinates and B-values of Table 5.

100. The model of claim 98, wherein at least about 50% of the structure has an average root-mean-square (RMSD) of less than about 1.5Å for the conserved amino acid residues in the acceptor binding site.

101. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 70% identical to the conserved amino acid residues of the acceptor binding site of E. coli MurG.

102. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 80% identical to the conserved amino acid residues of the acceptor binding site of E. coli MurG.

103. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 90% identical to the conserved amino acid residues of the E. coli MurG.

104. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 95% identical to the conserved amino acid residues of the acceptor binding site of the E. coli MurG.

105. The model of claim 98, wherein the acceptor binding site comprises an amino acid sequence that is at least about 70% identical to the amino acid sequence selected from the group consisting of *Escherichia coli, Bacillus subtilis, Aquefex aeolicus, Borrelia burgdorferi, Chlamydia pneumoniae, Chlamydia trachomatis, Enterococcus faecais, Enterococcus hirae, Haemophilus influenzae, Helicobacter pylori J99, Helicobacter pylori, Mycobacterium tuberculosis, Porphyromonas gingivalis, Rickettsia prowazekii,Streptomyces coelicolor, Streptomyces collinus, Streptococcus pneumoniae, Synechocystis* sp. (strain PCC6803), *Thermotoga maritime,* and *Treponema pallidum.*

106. The model of claim 98, wherein the atomic coordinates are generated by the method comprising the steps of:

a) providing a MurG protein in a crystalline form:

b) generating an electron-density map of said crystalline MurG protein; and

c) analyzing the electron-density map to produce the atomic coordinates.

107. The model of claim 98, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.

108. A model of a membrane association site of a UDP-glycosyltransferase (MurG) protein, wherein the model represents a three-dimensional structure that substantially conforms to the atomic coordinates of Table 6.

109. The model of claim 108, wherein the structure substantially conforms to the atomic coordinates and B-values of Table 4.

110. The model of claim 108, wherein at least about 50% of the structure has an average root-mean-square (RMSD) of less than about 1.5Å for conserved amino acid residues in the E. coli membrane association site.

111. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 70% identical to the conserved amino acid residues of the membrane association site of E. coli MurG.

112. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 80% identical to the conserved amino acid residues of the membrane association site of the E. coli MurG.

113. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 90% identical to the conserved amino acid residues of the membrane association site of the E. coli MurG.

114. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 95% identical to the conserved amino acid residues of a membrane association site of the E. coli MurG.

115. The model of claim 108, wherein the membrane association site comprises an amino acid sequence that is at least about 70% identical to the amino acid sequence from organisms selected from the group consisting of *Escherichia coli, Bacillus subtilis, Aquefex aeolicus, Borrelia burgdorferi, Chlamydia pneumoniae, Chlamydia trachomatis, Enterococcus faecais, Enterococcus hirae, Haemophilus influenzae, Helicobacter pylori J99, Helicobacter pylori, Mycobacterium tuberculosis, Porphyromonas gingivalis, Rickettsia prowazekii,Streptomyces coelicolor, Streptomyces collinus, Streptococcus pneumoniae, Synechocystis* sp. (strain PCC6803), *Thermotoga maritime,* and *Treponema pallidum.*

116. The model of claim 108, wherein the model is a computer image generated by a computer-readable medium encoded with a set of three-dimensional coordinates of the three-dimensional structure, wherein, using a graphical display software program, the three-dimensional coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a three-dimensional image.

117. A computer-assisted method of structure based drug design of bioactive compounds, comprising the steps of:

(a) providing a model of a UDP-glycosyltransferase (MurG)protein or a donor nucleotide binding site, acceptor binding site or membrane association site; and

(b) designing a chemical compound using said model.

118. The method of claim 117, further comprising the step of synthesizing the chemical compound.

119. The method of claim 118, further comprising the step of evaluating the bioactivity of the synthesized chemical compound.

120. The method of claim 118, wherein the model of the UDP-glycosyltransferase (MurG) protein represents a three-dimensional structure comprising the atomic coordinates listed in Table 1.

121. The method of claim 118, wherein the model of the donor nucleotide binding site represents a three-dimensional structure comprising the atomic coordinates Table 4.

122. The method of claim 118, wherein the model of the acceptor binding site represents a three-dimensional structure comprising the atomic coordinates in Table 5.

123. The method of claim 118, wherein the model of the membrane association site represent a three-dimensional structure comprising the atomic coordinates in Table 6.

124. The method of claim 118, wherein the model comprises a computer image generated when the atomic coordinates listed in Table 1 are analyzed on a computer using a graphical display software program to create an electronic file of the image and visualizing the electronic file on a computer capable of representing the electronic file as a three-dimensional image.

125. The method of claim 118, wherein the step of designing comprises computational screening of one or more databases of chemical compounds in which the three dimensional structure of said compounds are known.

126. The method of claim 125, further comprising interacting a compound identified by the screening step with the model by computer.

127. The method of claim 118, wherein the step of designing comprises directed drug design.

128. The method of claim 118, wherein the step of designing comprises random drug design.

129. The method of claim 118, wherein the step of designing comprises grid-based drug design.

130. The method of claim 118, wherein the step of designing comprises selecting compounds which are predicted to mimic the three-dimensional structure of the three-dimensional structure of the MurG protein.

131. The method of claim 118, wherein the step of designing comprises selecting compounds which are predicted to bind to the three-dimensional structure of the MurG protein.

132. The method of claim 118, wherein the bioactivity is selected from the group consisting of inhibiting binding of a nucleotide donor compound to the MurG protein,

inhibiting binding of an acceptor compound to the MurG protein, or inhibiting association of the MurG Protein to a membrane.

133. A model of the three dimensional structure of a MurG protein , wherein the model is produced by the following method comprising the steps of:

(a) providing an amino acid sequence of a MurG protein and the amino acid sequence of the *Escherichia coli* MurG protein;

(b) identifying structurally conserved regions shared between the the MurG protein and the E. coli MurG protein; and

(c) determining atomic coordinates for the MurG protein by assigning the structurally conserved regions of the MurG protein to a three dimensional structure using a three dimensional structure of the MurG protein which substantially conforms to the atomic coordinates represented in Table 1, to derive a model of the three dimensional structure of the MurG protein amino acid sequence.

134. The model of claim 133, wherein the MurG protein amino acid sequence comprises the sequence of an amino acid sequence selected from the group consisting of the amino acid sequences of MurG proteins as deposited in the NCBI database and identified with Accession Nos. CAB51993, A71316, E70579, C71699, F70195, A43727, JC1275, BVECMG, CEECAM, O83535, Q9ZK59, CAB85280, AAF39020, BAA18775, AAD26629, CAB73295, P37585, Q9ZHA9, Q9ZHDC0, Q9ZBA5, Q9X4H4, Q9WY74, P74657, O06224, Q9Z702, O84766, O69552, )67238, O51708, O25770, O07670, O07109, P45065, CAB66324, AAC68356, AAF06830, P18579, P17443, P17952, P16457, P07862, AAE23178, AAD53936, CAA18668, CAA38869, CAA38868, CAA38867, CAA38866, AAD08196, BAA01453, BAA01455, BAA01454, AAD19042, CAA45558, CAA74235, AAD10537, AAD06652, AAC95450, CAA14869, AAC73201, AAC65509, AAC67113, AAC45636, CAB08640, AAC22793, AAC07193, BAA24357, CAB13395, BAA01355, AAB35538, 1904153C, 1808265B, 1808265A, CAA36866, CAA36869, CAA36868, CAA36867, CAA36776, and AAA99436.

135. A composition for inhibiting the activity of a glycosyltransferase comprising a compound that inhibits the activity of a glycosyltransferase, wherein the compound is identified by the method comprising the steps of:

(a) providing a three-dimensional structure of a MurG protein;

(b) using the three-dimensional structure of the MurG protein to design a chemical compound that inhibits activity of a glycosyltransferase;

(c) synthesizing the chemical compound; and

(d) evaluating the ability of the chemical compound to inhibit the activity of a glycosyltransferase.

136. e composition of claim 135, wherein the glycosyltransferase is a MurG protein.

137. The composition of claim 135, wherein the three-dimensional structure of the MurG protein substantially conforms to atomic coordinates represented by Table 1.

138. The composition of claim 135, wherein the compound is selected from the group consisting of an inorganic and an organic compound.

139. The composition of claim 135, wherein the compound is a substituted pyrimidine analogs

140. The composition of claim 135, wherein the compound is selected from the group consisting of an analog of a MurG protein, a substrate analog of a MurG protein, a donor molecule analog of a MurG protein, and a membrane analog of a MurG protein.

141. The composition of claim 135, further comprising a component selected from the group consisting of an excipient an adjuvant, and a carrier.

142. A composition for stimulating the activity of a glycosyltransferase comprising a compound that stimulates the activity of a glycosyltransferase, wherein the compound is identified by the method comprising the steps of:

(a) providing a three-dimensional structure of a MurG protein;

(b) using the three-dimensional structure of the MurG protein to design a chemical compound that inhibits activity of a glycosyltransferase;

(c) synthesizing the chemical compound; and

(d) evaluating the ability of the chemical compound to stimulate the activity of a glycosyltransferase.

143. A method to determine a three-dimensional structure of a MurG protein comprising the steps of:

(a) providing an amino acid sequence of a MurG protein, wherein the three-dimensional structure of the MurG protein is not known;

(b) analyzing the pattern of folding of the amino acid sequence in a three-dimensional conformation by fold recognition; and

(c) comparing the pattern of folding of the MurG protein amino acid sequence with the three dimensional structure of the E. coli MurG protein, wherein the three-dimensional structure of the E. coli MurG protein substantially conforms to the atomic coordinates represented in Table 1.

144. A method to derive a model of the three-dimensional structure of a MurG protein comprising the steps of:

(a) providing an amino acid sequence of a MurG protein;

(b) identifying structurally conserved regions shared between the MurG protein and the E. coli MurG protein;

(c) determining atomic coordinates for the MurG protein structure by assigning the structurally conserved regions of the MurG protein to a three-dimensional structure using a three dimensional structure of the E. coli MurG protein based on atomic coordinates represented in Table 1 to derive a model of the three dimensional structure of the MurG protein amino acid sequence.

145. The method of claim 144, further comprising assigning atomic coordinates for side chains of said MurG protein by determining sterically allowable positions using a library of rotamers.

146. A method to derive a three dimensional structure of a crystallized MurG protein comprising the steps of:

(a) comparing the Patterson function of a crystallized MurG protein with the Patterson function of crystalline E. coli MurG protein to produce an electron-density map of the crystallized MurG protein; and

(b) analyzing the electron-density map to produce the three dimensional structure of the crystallized MurG protein.

147. The method of claim 146, further comprising the step of rotating the Patterson function of the crystallized MurG protein on the Patterson function of the crystalline E coli MurG protein to determine the correct orientation of the crystallized MurG protein in a crystal of said crystallized MurG protein to identify the initial phases of the crystallized MurG protein.

148. The method of claim 146, further comprising the step of electronically stimulating the three dimensional structure of the crystallized MurG protein to derive a computer image of the three dimensional structure of the crystallized MurG protein.